

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: September 7, 2002, 22:34:06 ; Search time 265.48 Seconds
(without alignments)
782.532 Million cell updates/sec

Title: US-09-719-017A-1

Perfect score: 121
Sequence: 1 gaattccctgtgacaatta.....tatctaagaataacttaca 121

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_032802:*

- 1: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121	100.0	121	21	AAZ45324
2	121	100.0	1793	21	AAA47190
3	121	100.0	1793	21	AAZ45325
4	59.2	48.9	693	12	AAQ11856
5	54.8	45.3	59	15	AAQ53901
6	54.8	45.3	60	21	AAA12878
7	50	41.3	59	15	AAQ53902
8	50	41.3	59	21	AAA12877
9	44	36.4	77	16	AAI00582

10	44	36.4	77	18	AAI73712	Tryptophan promote
11	43.6	36.0	357	21	AAI64251	trp promoter used
12	43.6	36.0	357	21	AAA95073	trp promoter. Uni
13	43.2	35.7	1519	20	AAV81508	High expression tr
14	43.2	35.7	1519	21	AAA73025	Translucemase n
15	42.8	35.4	63	6	AAI50137	trp promoter. AA
16	42.2	34.9	305	14	AAQ49722	trp promoter EcORI
17	42	34.7	47	9	AAI80245	Sequence of synthe
18	42	34.7	74	13	AAQ31933	trp-promoter [M1 (
19	42	34.7	86	3	AAQ20110	trp promoter. SYN
20	42	34.7	102	11	AAQ03558	EcORI-PstI fragmen
21	42	34.7	103	6	AAI50704	Synthetic DNA sequ
22	42	34.7	103	8	AAI70717	Sequence of a synt
23	42	34.7	103	9	AAI80723	Human SP5 #19. Ho
24	42	34.7	103	10	AAI93089	Synthetic tryptoph
25	42	34.7	105	9	AAI81566	trp promoter III g
26	42	34.7	107	6	AAI50168	Synthetic promoter
27	42	34.7	107	7	AAI60080	Sequence of synthe
28	42	34.7	107	8	AAI70163	Sequence of synthe
29	42	34.7	107	8	AAI70602	trp promoter used
30	42	34.7	107	12	AAI3118	Synthetic trp prom
31	42	34.7	107	16	AAQ79932	Sequence of synthe
32	42	34.7	111	7	AAI60088	Synthetic trp pr
33	42	34.7	111	12	AAI3116	Sequence of trp pr
34	42	34.7	137	8	AAI70250	Plasmid fragment.
35	42	34.7	141	3	AAI20014	Modified trp promo
36	42	34.7	151	22	AAI69044	Components of E. c
37	42	34.7	166	10	AAI91224	Sequence of synthe
38	42	34.7	167	7	AAI60089	Synthetic trp prom
39	42	34.7	167	12	AAI3117	EcORI-ClaI fragmen
40	42	34.7	167	12	AAI4900	E. coli trp promot
41	42	34.7	168	13	AAQ28382	EcORI-ClaI fragmen
42	42	34.7	172	12	AAQ13327	PAR153 partial seq
43	42	34.7	172	14	AAQ36948	V-min gene detecti
44	42	34.7	172	15	AAQ65387	
45	42	34.7	264	13	AAQ25936	POCF A chain expre

ALIGNMENTS

RESULT 1	
AAZ45324	AAZ45324 standard; DNA; 121 BP.
XX	XX
AC	AAZ45324;
XX	XX
DT	27-MAR-2000 (first entry)
XX	XX
DE	Nucleotide sequence of the trp promoter.
XX	XX
KW	Tryptophan promoter; trp promoter; heterologous protein expression;
KM	Escherichia coli W; industrial protein production; enzyme; nitrilase; ss.
XX	XX
OS	Unidentified.
XX	XX
PN	WO964607-A1.
XX	XX
PD	16-DEC-1999.
XX	XX
PE	08-JUN-1999; 99MO-FR01343.
XX	XX
PR	10-JUN-1998; 98PR-0007474.
XX	XX
PA	(RHON) RHONE-POULENC NUTRITION ANIMALE.
XX	XX
PI	Pierrard J, Guitton C, Favre-Bulle O;
XX	XX
DR	WPI; 2000-097541/08.
XX	XX
PT	Industrial production of heterologous proteins in Escherichia coli
XX	XX
	strain W, particularly for expressing enzymes

PS C1alm 15; Page 36; 52pp; French.

XX The present sequence represents the tryptophan promoter (P_{trp} promoter).
CC The promoter was extracted from plasmid pRPA6BCAT6 by restriction digest.
CC The promoter is used to control the expression of a heterologous
CC protein in an expression cassette which is used to modify a strain of
CC *Escherichia coli* W. The modified strain is then used for industrial
CC production of heterologous proteins. Specifically, the promoter was
CC used to control the expression of an *Alcaligenes nitrilase* gene.
CC The method is especially used to produce proteins of relatively
CC low value, preferably enzymes and specifically nitrilases.
SQ Sequence 121 BP; 37 A; 27 C; 23 G; 34 T; 0 other;

Query Match 100.0%; Score 121; DB 21; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaattccctgttgacaatcatcgaactgaactagtagttagcagcgttgctgcag 60
DB 1 gaattccctgttgacaatcatcgaactgaactagtagttagcagcgttgctgcag 60
OY 61 tcgacctgcagcgaagcttgaggcatatcgaatcgaatgtgtatctaaagaaatactac 120
DB 61 tcgacctgcagcgaagcttgaggcatatcgaatcgaatgtgtatctaaagaaatactac 120
OY 121 a 121
DB 121 a 121

RESULT 2
AAA47190
ID AAA47190 standard; DNA: 1793 BP.

AC AAA47190;

DT 03-OCT-2000 (first entry)

DE Nucleotide sequence of the expression cassette of pRPA-BCAT41.

KW Methionine: 2-hydroxy-4-methylthiobutanoic acid; nitrilase;

KM nitrile hydratase; amidase; pRPA-BCAT41; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 123..1193

FT CDS /*tag- a

PN MO200036120-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99MO-FR03089.

PR 11-DEC-1998; 98FR-0015849.

PR 19-JUL-1999; 99FR-0009489.

PA (RHON) RHONE-POULENC ANIMAL NUTRITION SA.

PI Favre-Bulle O, Pierrard J, Batisse Debitte N;

DR WPI; 2000-431598/37.

DR P-PSDB; AAY93908.

XX Selecting sequences encoding enzymes involved in methionine synthesis,

XX useful for hydrolysis of nitrile groups, by transforming methionine

XX auxotrophs and selection for growth

XX Example 1; Page 27-29; 38pp; French.

CC The specification describes a process for the selection and/or isolation
CC of DNA sequences that encode enzymes involved in bioconversion of
CC substrates to methionine or its derivatives such as
CC 2-hydroxy-4-methylthiobutanoic acid. DNA fragments are cloned into
CC a microbial expression vector and recombinant vectors used to transform
CC a host that is auxotrophic for methionine (Met). The cells are cultured
CC in medium containing an adequate amount of substrate and microbes able
CC to grow on this medium are selected and/or isolated. DNA sequences
CC involved in conversion of substrates are then isolated and/or identified.
CC The method is used to identify DNA sequences encoding nitrilases, nitrile
CC hydratases or amidases. Nitrilases are useful in many synthetic process
CC that require hydrolysis of nitrile groups, e.g. for production of the
CC hydroxy analogue of Met. The present sequence is the nucleotide sequence
CC of the expression cassette of pRPA-BCAT41.

SQ Sequence 1793 BP; 412 A; 527 C; 478 G; 376 T; 0 other;

Query Match 100.0%; Score 121; DB 21; Length 1793;
Best Local Similarity 100.0%; Pred. No. 7.3e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaattccctgttgacaatcatcgaactgaactagtagttagcagcgttgctgcag 60
DB 1 gaattccctgttgacaatcatcgaactgaactagtagttagcagcgttgctgcag 60
OY 61 tcgacctgcagcgaagcttgaggcatatcgaatcgaatgtgtatctaaagaaatactac 120
DB 61 tcgacctgcagcgaagcttgaggcatatcgaatcgaatgtgtatctaaagaaatactac 120
OY 121 a 121
DB 121 a 121

RESULT 3
AA245325
ID AA245325 standard; DNA: 1793 BP.

AC AA245325;

DT 27-MAR-2000 (first entry)

DE Nucleotide sequence of an expression cassette encoding a nitrilase.

KW Tryptophan promoter; P_{trp} promoter; heterologous protein expression;

KM *Escherichia coli* W; industrial protein production; enzyme; nitrilase; ss.

OS Synthetic.

XX faecalis.

XX Key Location/Qualifiers

FT CDS 123..1193

FT CDS /*tag- a

FT CDS /product= "nitrilase"

PN MO964607-A1.

PD 16-DEC-1999.

PF 08-JUN-1999; 99MO-FR01343.

PR 10-JUN-1998; 98FR-0007474.

PA (RHON) RHONE-POULENC NUTRITION ANIMALE.

PI Pierrard J, Guitton C, Favre-Bulle O;

DR WPI; 2000-097541/08.

DR P-PSDB; AAY54121.

XX Industrial production of heterologous proteins in *Escherichia coli*

XX strain W, particularly for expressing enzymes

```
XX XX Example 1; Page 36-38; 52pp; French.
PS XX
XX CC The present sequence represents an expression cassette comprising
CC the tryptophan promoter (Ptrp promoter) and DNA encoding an Alcaligenes
CC faecalis ATCC8750 nitrilase (nitB). The nitrilase polynucleotide and the
CC promoter sequence were extracted from plasmid pRP46BCA76 by restriction
CC digest. The Ptrp promoter is used to control the expression of a
CC heterologous protein in an expression cassette which is used to modify
CC a strain of Escherichia coli W. The modified strain is then used for
CC industrial production of heterologous proteins. Specifically, the
CC promoter is used to control the expression of an Alcaligenes nitrilase
CC gene. The method is especially used to produce proteins of relatively
CC low value, preferably enzymes and specifically nitrilases.
SQ XX Sequence 1793 BP; 412 A; 527 C; 478 G; 376 T; 0 other;

Query Match          100.0%; Score 121; DB 21; Length 1793;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaattccctgtgacaattatcatcgactagtagttagcagcagctgtgctgagg 60
DB 1 gaattccctgtgacaattatcatcgactagtagttagcagcagctgtgctgagg 60

QY 61 tcgacctgcagcaagcttgtagcatatcatcaatctgttatctagaagaataacttac 120
DB 61 tcgacctgcagcaagcttgtagcatatcatcaatctgttatctagaagaataacttac 120

QY 121 a 121
DB 121 a 121

RESULT 4
AAQ11856
ID AAQ11856 standard; DNA: 695 BP.
XX
XX AC AAQ11856;
XX
XX DT 31-JUL-1991 (first entry)
XX
XX DE Sequence of plasmid pHBcat encoding VHB structural haemoglobin gene.
XX
XX KM Haemoglobin; fermentation; brewing; ds.
XX
XX OS Vitreoscilla sp.
XX
XX FH Key Location/Qualifiers
XX FT misc_signal 1..91
XX FT /*tag= a
XX FT /*tag= trp promoter and synthetic RBS
XX FT mat_peptide 92..529
XX FT /*tag= b
XX FT /*label= Vitreoscilla structural gene
XX
XX PN W09106641-A.
XX
XX PD 16-MAY-1991.
XX
XX PF 26-OCT-1990; 90WO-US06083.
XX
XX PR 30-OCT-1989; 89US-0429093.
XX
XX PA (CALY ) CALIF INST OF TECHN.
XX
XX PI Bailey JE, Khosla CS;
XX
XX DR WPI; 1991-164191/22.
XX
XX PT Enhancing cell growth - preparing foreign proteins, by
PT co-expressing haemoglobin gene.
```

```
XX XX Disclosure; Page 47; 84pp; English.
PS XX
XX CC By coexpressing a desired DNA sequence in a plasmid with the
CC haemoglobin structural gene, expression may be regulated by the
CC level of dissolved oxygen, presence of CAP-CAP and/or a complex
CC nitrogen source. The method is especially useful in the production
CC of haemoglobins and metabolites, fermentation, brewing, enzymatic
CC degradation, waste treatment etc.
SQ XX Sequence 695 BP; 184 A; 147 C; 176 G; 186 T; 2 other;

Query Match          48.9%; Score 59.2; DB 12; Length 695;
Best Local Similarity 95.3%; Pred. No. 2.5e-09;
Matches 61; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 aattccctgtgacaattatcatcgactagtagttagcagcagctgtgctgagg 61
DB 3 attccctgtgacaattatcatcgactagtagttagcagcagctgtgctgagg 62

QY 62 cgac 65
DB 63 cgac 66

RESULT 5
AAQ53901
ID AAQ53901 standard; DNA: 59 BP.
XX
XX AC AAQ53901;
XX
XX DT 22-JUN-1994 (first entry)
XX
XX DE Trp promoter used in expression vector.
XX
XX KM Saporin; restenosis; melanoma; carcinoma; ovarian cancer;
XX cytotoxin; fusion protein; targeting; internalisation; ligand;
XX receptor; cell surface; ss.
XX
XX OS Synthetic.
XX
XX PN W09325688-A.
XX
XX PD 23-DEC-1993.
XX
XX PF 14-JUN-1993; 93WO-US05702.
XX
XX PR 16-JUN-1992; 92US-0901718.
XX
XX PA (PRIZ-) PRIZM PHARM INC.
XX PA (WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
XX
XX PI Baird JA, Barthelamy I, Lappi DA, Sosnowski BA;
XX
XX DR WPI; 1994-007545/01.
XX
XX PT Recombinant fusion proteins contg. saporin - having an N-terminal
PT extension to permit recombinant expression and opt. to target the
PT protein to target cells
XX
XX PS Example 2; Page 33; 62pp; English.
XX
XX CC Recombinant fusion proteins containing saporin can be used for
XX treating diseases such as restenosis, human melanomas and human
XX ovarian carcinomas. The proteins comprise saporin with an N-
XX terminal extension, the saporin containing protein being cytotoxic
XX upon internalisation by a eukaryotic cell. The N-terminal extension
XX may include a ligand e.g. basic fibroblast growth factor (bFGF),
XX that specifically interacts with a cell surface protein, thus
XX specific cells can be targeted. The N-terminal extension renders
XX the resulting saporin containing protein sufficiently non-cytotoxic
XX to allow recombinant expression. The trp promoter was used in
```

CC	constructs to regulate expression of saporin/DFGF fusion proteins.
CC	Sequence 59 BP; 17 A; 14 C; 11 G; 17 T; 0 other;
Query Match	45.3%; Score 54.8; DB 15; Length 59;
Best Local Similarity	96.6%; Pred. No. 3.6e-08;
Matches	56; Conservative 0; Mismatches 2; Indels 0; Gaps
OY	2 aattccctgtgaacattcaatcagacagcttaactagtaacagcagctgtcag 59
DB	2 attccctgtgacaattcaatcagacagcttaactagtaacagcagctgtcag 59
RESULT 6	
AA12878	
ID	AA12878 standard; DNA; 60 BP.
XX	AA12878:
XX	18-JUL-2000 (first entry)
XX	TTP promoter, SEQ ID NO:62.
XX	
KW	Targetted gene delivery; fibroblast growth factor receptor;
KW	FGFR-binding protein; nucleic acid binding protein;
KW	receptor-internalised ligand; cytoxin; saporin; gene therapy;
KW	cytotoxic; antiproliferative; cancer; melanoma; diabetic retinopathy;
KW	rheumatoid arthritis; restenosis; Dupuytren's contracture; psoriasis;
KW	eczema; promoter; alpha-actin; alpha-crystallin; ribosome binding site;
XX	ss.
XX	Undentified.
XX	
XX	US6037329-A.
XX	
XX	14-MAR-2000.
XX	
XX	24-SEP-1996; 96US-0718904.
XX	
XX	15-MAR-1994; 94US-0213446.
XX	15-MAR-1994; 94US-0213447.
XX	29-AUG-1994; 94US-0297961.
XX	13-SEP-1994; 94US-0305771.
XX	16-MAY-1995; 95US-0441979.
XX	
XX	(SELF-) SELECTIVE GENETICS INC.
XX	
XX	Chandler LA, Sosnowski BA, Baird JA;
XX	
XX	WPI, 2000-292008/25.
XX	
XX	Gene delivery system, useful for treating or preventing cancer and
XX	rheumatoid arthritis, comprises receptor-internalized ligand linked to
XX	nucleic acid binding domain and nucleic acid
XX	
XX	Example 6; Column 145; 131pp; English.
XX	
XX	The invention relates to a novel gene delivery composition for the
XX	targeted delivery of cytotoxins or prodrug-converting enzymes to
XX	proliferating cells. The gene delivery composition comprises a protein
XX	that binds the fibroblast growth factor receptor (FGFR) which is fused
XX	or chemically conjugated to a nucleic acid binding domain. The nucleic
XX	acid binding domain is complexed with a suitable expression construct
XX	encoding a cytotoxin such as saporin. One or more linkers may join the
XX	FGFR-binding protein to the nucleic acid binding protein. These are
XX	selected to increase the specificity, toxicity, solubility, serum
XX	stability or intracellular availability, and may serve to promote
XX	condensation of nucleic acids for delivery to a cell. The fusion protein
XX	binds to FGFR and is internalised by cells that carry this receptor. The
XX	gene delivery composition is used for the therapeutic alteration of the
XX	function, gene expression and viability of cells. In particular, it may
XX	be used for the treatment and prevention of cell proliferative

CC	disorders, for example after eye surgery, melanoma and many other sorts
CC	of cancer, rheumatoid arthritis, restenosis, Dupuytren's contracture,
CC	diabetic retinopathy, psoriasis and eczema. The gene delivery
CC	compositions of the invention have high specificity for particular cells
CC	and can deliver larger amounts of DNA compared to prior art methods.
CC	Sequence AA112925 represents the human alpha-actin promoter, and
CC	sequences AA112923-112924 represent PCR primers used to amplify this
CC	promoter. Sequence AA112934 represents the human alpha-crystallin
CC	promoter, which was generated using PCR primers AA112926-112933. Sequence
CC	AA112878 represents a Trp gene promoter, and sequence AA112877 represents
CC	the cII ribosome binding site of bacteriophage lambda. All these elements
CC	may be incorporated into the cytotoxin-encoding DNA construct to be
CC	delivered to the cell. Sequence AA112876 represents an oligonucleotide of
CC	undefined function.
XX	
SQ	Sequence 60 BP; 17 A; 14 C; 12 G; 17 T; 0 other;
XX	
Query Match	45.3%; Score 54.8; DB 21; Length 60;
Best Local Similarity	96.6%; Pred. No. 3.7e-08;
Matches 56; Conservative	0; Mismatches 2; Indels 0; Gaps 0;
Oy	2 aatccctgtgcgaattaatcatcgacactgactagtcagcagctggctgcag 59
Db	3 attccctgtgtgcgaattaatcatcgacactgactagtcagcagctggctgcag 60
RESULT 7	
AA053902	
ID	AA053902 standard; DNA; 59 BP.
AC	AA053902;
XX	
DT	22-JUN-1994 (first entry)
DE	
XX	
XX	Landa cII ribosome binding site used in expression vector.
XX	
XX	Saporin; restenosis; melanoma; carcinoma; ovarian cancer;
KW	cytotoxin; fusion protein; targeting; internalisation; ligand;
KW	receptor; cell surface; ss.
XX	
OS	Lambda phage.
XX	
PN	WO9325688-A.
XX	
PD	23-DEC-1993.
XX	
PF	14-JUN-1993; 93WO-US05702.
XX	
PR	16-JUN-1992; 92US-0901718.
XX	
PA	(PRIZM PHARM INC.
PA	(WHITE-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
XX	
PI	Baird JA, Barthelemy I, Lappi DA, Sosnowski BA.
DR	WPI; 1994-007545/01.
XX	
XX	
PT	Recombinant fusion proteins contg. saporin - having an N-terminal
PT	extension to permit recombinant expression and opt. to target the
PT	protein to target cells
XX	
XX	
PS	Example 2; Page 33; 62pp; English.
XX	
CC	Recombinant fusion proteins containing saporin can be used for
CC	treating diseases such as restenosis, human melanomas and human
CC	ovarian carcinomas. The proteins comprise saporin with an N-
CC	terminal extension, the saporin containing protein being cytotoxic
CC	upon internalisation by a eukaryotic cell. The N-terminal extension
CC	may include a ligand e.g. basic fibroblast growth factor (bFGF),
CC	that specifically interacts with a cell surface protein, thus
CC	specific cells can be targeted. The N-terminal extension renders
CC	the resulting saporin containing protein sufficiently non-cytotoxic
CC	

to allow recombinant expression. The lambda CII ribosome binding site was used in constructs for expressing saporin/bFGF fusion proteins.

Sequence 59 BP; 20 A; 11 C; 10 G; 18 T; 0 other:

Query Match 41.3%; Score 50; DB 15; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ccaagcttgagcatcacatcaatgtttatcctaagaataacttaca 121
Db 6 ccaagcttggcatcacatcaatcaatgtttatcctaagaataacttaca 55

RESULT 8

AAA12877
ID AAA12877 standard; DNA; 59 BP.

AC AAA12877;
XX
DT 18-JUL-2000 (first entry)

DE Bacteriophage lambda cII ribosome binding site, SEQ ID NO:61.

XX Targetted gene delivery; fibroblast growth factor receptor;
KM FGFR-binding protein; nucleic acid binding protein;
KM receptor-internalised ligand; cytoxin; saporin; gene therapy;
KM cytotoxic; antiproliferative; cancer; melanoma; diabetic retinopathy;
KM rheumatoid arthritis; restenosis; Dupuytren's contracture; psoriasis;
KM eczema; promoter; alpha-actin; alpha-crystallin; ribosome binding site;
XX ss.

OS Bacteriophage lambda.

XX US6037329-A.

PD 14-MAR-2000.

PF 24-SEP-1996; 96US-0718904.

XX 15-MAR-1994; 94US-0213446.
PR 15-MAR-1994; 94US-0213447.
PR 29-AUG-1994; 94US-0297961.
PR 13-SEP-1994; 94US-0305771.
PR 16-MAY-1995; 95US-0441979.

XX (SELE-) SELECTIVE GENETICS INC.

PI Chandler LA, Sosnowski BA, Baird JA;

DR WPI: 2000-292008/25.

PT Gene delivery system, useful for treating or preventing cancer and
PT Rheumatoid arthritis, comprises receptor-internalized ligand linked to
PT nucleic acid binding domain and nucleic acid -
XX

PS Example 6; Column 65-66; 131pp; English.

XX The invention relates to a novel gene delivery composition for the
CC targeted delivery of cytotoxins or prodrug-converting enzymes to
CC proliferating cells. The gene delivery composition comprises a protein
CC that binds the fibroblast growth factor receptor (FGFR) which is fused
CC or chemically conjugated to a nucleic acid binding domain. The nucleic
CC acid binding domain is complexed with a suitable expression construct
CC encoding a cytotoxin such as saporin. One or more linkers may join the
CC FGFR-binding protein to the nucleic acid binding protein. These are
CC selected to increase the specificity, toxicity, solubility, serum
CC stability or intracellular availability, and may serve to promote
CC condensation of nucleic acids for delivery to a cell. The fusion protein
CC binds to FGFR and is internalised by cells that carry this receptor. The
CC gene delivery composition is used for the therapeutic alteration of the

CC function, gene expression and viability of cells. In particular, it may
CC be used for the treatment and prevention of cell proliferative
CC disorders, for example after eye surgery, melanoma and many other sorts
CC of cancer, rheumatoid arthritis, restenosis, Dupuytren's contracture,
CC diabetic retinopathy, psoriasis and eczema. The gene delivery
CC compositions of the invention have high specificity for particular cells
CC and can deliver larger amounts of DNA compared to prior art methods.
CC Sequence AAA12925 represents the human alpha-actin promoter, and
CC sequences AAA12923-A12924 represent PCR primers used to amplify this
CC promoter. Sequence AAA12934 represents the human alpha-crystallin
CC promoter, which was generated using PCR primers AAA12926-A12933. Sequence
CC AAA12878 represents a TRP gene promoter, and sequence AAA12877 represents
CC the CII ribosome binding site of bacteriophage lambda. All these elements
CC may be incorporated into the cytotoxin-encoding DNA construct to be
CC delivered to the cell. Sequence AAA12876 represents an oligonucleotide of
CC undefined function.

SO Sequence 59 BP; 20 A; 11 C; 10 G; 18 T; 0 other:

Query Match 41.3%; Score 50; DB 21; Length 59;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 ccaagcttgagcatcacatcaatgtttatcctaagaataacttaca 121
Db 6 ccaagcttggcatcacatcaatcaatgtttatcctaagaataacttaca 55

RESULT 9

AAT00582
ID AAT00582 standard; DNA; 77 BP.

AC AAT00582;

DT 28-MAY-1996 (first entry)

DE TRP promoter.

KM TRP; anti-phosphoglycerate mutase; PGAM; antibody; IgG; isoenzyme; ds.

OS Escherichia coli.

PN JP07258299-A.

PD 09-OCT-1995.

PF 25-MAR-1994; 94JP-0079867.

XX 25-MAR-1994; 94JP-0079867.

PA (ORIV) ORIENTAL YEAST CO LTD.

DR WPI: 1995-380078/49.

PT Anti-phosphoglycerate mutase isozyme specific IgG antibodies - used
PT to detect and distinguish between M and B type isozyme(s)

PS Disclosure; Fig 2; 12pp; Japanese.

XX This sequence represents the TRP promoter. This sequence was used in an
CC expression vector to express anti-phosphoglycerate mutase (PGAM) M and B
CC type isozyme specific IgG antibodies. These antibodies were termed MM
CC and BB respectively. The antibodies MM and BB can be used to detect and
CC distinguish between the two PGAM isozymes. They can also be used in
CC various diagnostic agents.

SO Sequence 77 BP; 26 A; 16 C; 15 G; 20 T; 0 other:

Query Match 36.4%; Score 44; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PS Disclosure; Page 48-50; 74pp; Japanese.
 XX
 CC The present invention describes a method for producing active
 CC transglutaminase from denatured enzyme. The method comprises: (1) forming
 CC an intermediate structure of the enzyme having transglutaminase activity
 CC under acidic conditions in an aqueous medium; and (ii) forming a higher-
 CC level structure of the enzyme having transglutaminase activity under
 CC neutral conditions in an aqueous medium. The method can be used for
 CC industrial production of active transglutaminase from denatured material
 CC (such as recombinant transglutaminase) which can be used in the food
 CC industry for the production of gelled foods such as jellies, yoghurts
 CC and cheeses, and for the production of gelled cosmetics. The present
 CC sequence encodes a transglutaminase which is used in the exemplification
 CC from the present invention.
 SQ Sequence 1519 BP; 355 A; 350 C; 387 G; 427 T; 0 other;

Query Match 35.7%; Score 43.2; DB 21; Length 1519;
 Best Local Similarity 93.8%; Pred. No. 0.00035;
 Matches 45; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 tccctgtgacataatcatcgcgaactagttactagtagcagcgtt 51
 Db 2 tccctgtgacataatcatcgcgaactagttactagtagcagcgtt 49

RESULT 15

AA50137
 ID AA50137 standard; DNA; 63 BP.

AC AA50137;

DT 23-OCT-1991 (first entry)

DE Ttp promoter.

XX Promoter; ss.

KW

XX

Key

FT -35_signal

FT -10_signal

FT RBS

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

Location/Qualifiers
 5..10
 /*cag- a
 28..33
 /*cag- b
 55..58
 /*tag- C
 /label- Shine-Dalgarno

EP152830-A.

PD 28-AUG-1985.

XX

PF 31-JAN-1985; 85EP-0100976.

XX

PR 02-FEB-1984; 84JP-0018133.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Claim 10; Page 26; 38pp; English.
 The ttp promoter is used in the construction of novel vectors
 which are used for more efficient protein synthesis in a
 transformed host.

Sequence 63 BP; 22 A; 13 C; 11 G; 17 T; 0 other;

Query Match 35.4%; Score 42.8; DB 6; Length 63;
 Best Local Similarity 95.7%; Pred. No. 0.00024;
 Matches 44; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 cccgttgacataatcatcgcgaactagttactagtagcagcgtt 51
 Db 1 cccgttgacataatcatcgcgaactagttactagtagcagcgtt 46

Search completed: September 8, 2002, 00:42:25
 Job time: 7699 sec